Amendments to the Specification:

Please amend the paragraph (section) beginning on page 23, at line 19 as shown below:

~~The algorithm can be used via the Internet at: http://jsl1.chem.wayne.edu/Hyther/hytherm1main.html.~~ The algorithm may be written in FORTRAN 77 and run on UNIX environment or other languages and environments.

Please amend the paragraph (section) beginning on page 24, at line 2 as shown below:

The algorithm may be used to predict the thermodynamics of a set of literature measurements for molecular beacons (Bonnet et al., 1999). Molecular beacons are high specificity probes that are efficient for mutation analysis (Giensendorf et al., 1998) and multiplex detection of single nucleotide variations (Marras et al., 1999). The design and efficiency optimization of these beacons is helped by hybridization thermodynamics prediction. Bonnet et al. studied, the hybridization of the molecular beacon $^{5'}$CGC TCC, CAA, AAA, AAA, AAA, CCG AGC G$^{3'}$ to a set of four different targets including a perfect match duplex, and three different duplexes containing one mismatch. Free energy and enthalpy for duplex folding may be calculated using the DNA MFOLD program ~~(http://mfold2.wustl.edu/~mfold/dna/form1.cgi)~~. These parameters may then incorporated as secondary structure corrections in Figure 2a.

Please amend the paragraph (section) beginning on page 26, at line 7 as shown below:

Special corrections for single-stranded secondary structure and for surface corrections for hybridization arrays can be input. The units for input ΔG are kcal/mol. To determine estimates of single-strand folding energies, see Michael Zuker's RNA or DNA-MFOLD servers ~~(see http://mfold2.wsutl.edu/~mfold/dna/form1.cgi)~~. The current thermodynamic prediction software incorporates the special corrections for single-stranded secondary structure and for surface corrections for hybridization arrays.